



SEQUENCE LISTING

<110> Aharoni, Asaph
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O'Connell, Ann P.

<120> Fruit Flavour Related Genes And Use Thereof

<130> 2183-4916

<140> US/09/857,518

<141> 2002-03-29

<150> EP 98204018.0

<151> 1998-12-02

<150> EP 99200739.3

<151> 1999-03-12

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<170> PatentIn Ver. 2.1

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Val Pro Tyr Leu Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu	
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Arg Leu Arg Lys Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro	
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Phe Ser Met Glu Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val	
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Gln Val Asn Val Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser	
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His Lys Leu Ile Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp	
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175 180 185	
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Tyr Val Asp Gln Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala	
205 210 215 220	
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Thr Arg Arg Phe Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp	
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Glu Ala Lys Ser Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val	
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  Glu Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val
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  Pro Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp
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  Cys Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu
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  Gly Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly
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Ser	Lys	Thr	Asp	His	Glu	Pro	Asn	Val	Lys	Tyr	Ser	Arg	Met	Ala	Ile		
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 Ile Phe Asp

tgtcactttt tttttttttt ttttttgggg gcgcaaatgt tgtcttactt ggaattttat 1526

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gac tct tct ctc tcc gcg tcg gta tgt gcg gct ggg gat agc gct gcg 150
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 Tyr Ala Arg Asn His Val Phe Gly Asp Asp Val Val Ile Val Ala Ala
 40 45 50

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 Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg Gly Gly Phe Lys Tyr Thr
 55 60 65 70

tat gct gat gat ctc ctc gca cct gtc ctc aag gcc gtg gtt gag aaa 294
 Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu Lys Ala Val Val Glu Lys
 75 80 85

acc aat ctc aat ccc aag gaa gtc ggg gat att gtt gtc ggt acc gtc 342
 Thr Asn Leu Asn Pro Lys Glu Val Gly Asp Ile Val Val Gly Thr Val
 90 95 100

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 Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu Cys Arg Met Ala Ala Phe

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Tyr Ala Gly Phe Pro Glu Thr	Val Pro Val Arg Thr	Val Asn Arg Gln	
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      375              380              385              390

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Lys Asp Val Arg
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acc ctc ggc cgc cac ctg gca cgc cgc ctc gtt caa atc ggc gtc acc 254
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            95             100             105

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Ile Ala Gly Ala Tyr Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly
            125             130             135

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Gly Pro Asn Ser Asn Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr
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            175             180             185

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Val	Glu	Ser	Ala	Asp	Ala	Tyr	Leu	Phe	Ala	Gly	Pro	Ile	Phe	Asn	Asp		
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tgt	gtt	ctc	atg	aag	gat	ttc	ctc	tta	ggc	cta	gca	aag	aag	ctg	aag	1214	
Cys	Val	Leu	Met	Lys	Asp	Phe	Leu	Leu	Gly	Leu	Ala	Lys	Lys	Leu	Lys		
		365				370					375						
cat	aac	aac	act	gct	cat	gag	aac	tac	cgc	agg	atc	ttt	gtg	cct	gat	1262	
His	Asn	Asn	Thr	Ala	His	Glu	Asn	Tyr	Arg	Arg	Ile	Phe	Val	Pro	Asp		
380					385					390					395		
ggc	cac	cct	ctg	aag	gct	gca	ccc	aaa	gaa	cct	ttg	agg	gtt	aat	gtt	1310	
Gly	His	Pro	Leu	Lys	Ala	Ala	Pro	Lys	Glu	Pro	Leu	Arg	Val	Asn	Val		
				400					405					410			
ctg	ttc	aaa	cac	att	cag	aat	atg	ctg	tca	gct	gaa	acc	gct	gtg	att	1358	
Leu	Phe	Lys	His	Ile	Gln	Asn	Met	Leu	Ser	Ala	Glu	Thr	Ala	Val	Ile		
			415					420					425				
gct	gag	aca	ggg	gac	tca	tgg	ttt	aac	tgt	cag	aag	ctg	aaa	ttg	cca	1406	
Ala	Glu	Thr	Gly	Asp	Ser	Trp	Phe	Asn	Cys	Gln	Lys	Leu	Lys	Leu	Pro		

430	435	440	
ccc ggc tgc ggg tat gag ttc caa atg caa tat gga tca att ggt tgg			1454
Pro Gly Cys Gly Tyr Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp			
445	450	455	
tca gtt gga gca act ctt ggg tat gct cag gct gta cct gag aag cga			1502
Ser Val Gly Ala Thr Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg			
460	465	470	475
gtg att tct ttc att ggt gat ggg agc ttc cag gtg act gct caa gat			1550
Val Ile Ser Phe Ile Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp			
	480	485	490
gtg tcc aca atg att cga aat gga cag aga acc att att ttc ctg ata			1598
Val Ser Thr Met Ile Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile			
	495	500	505
aac aat ggt gga tac acc att gaa gtg gaa atc cat gat gga cca tac			1646
Asn Asn Gly Gly Tyr Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr			
	510	515	520
aat gtg atc aag aac tgg aac tac act gga ctg gtt gat gca atc cac			1694
Asn Val Ile Lys Asn Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His			
	525	530	535
aat ggg gaa ggc aag tgc tgg aca acc aag gtg cgt tgc gaa gag gag			1742
Asn Gly Glu Gly Lys Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu			
540	545	550	555
ctg att gaa gca ata gag act gca aat gga ccc aag aag gat agc ttc			1790
Leu Ile Glu Ala Ile Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe			
	560	565	570
tgc ttc att gag gtg att gtt cac aag gat gat acc agc aaa gag ttg			1838
Cys Phe Ile Glu Val Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu			
	575	580	585
ctt gag tgg ggg tct agg gtt tct gct gcc aac agc cgc cca cct aat			1886
Leu Glu Trp Gly Ser Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn			
	590	595	600
cct cag taaaactctc ctgtgtcata tgaaggcctt cattcacatt cacagattta			1942
Pro Gln			
605			
gatcaagcca agctcttgtg caaattttcc ttatgttttt cctgtcaact ggagaatggg			2002
gtctgtcaag ttttttttac actacagtga tttctggttt gtctgtatat ttccttctga			2062
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                                         1

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Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp Ala
      5              10              15

gca aga gat tca tct ggt gtt ctc tct ccc ttc agt ttc tcc aga agg 154
Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg Arg
      20              25              30

gaa acc gga gag aaa gac gtg acg ttc aaa gtg atg tac tgt ggg att 202
Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly Ile
      35              40              45

tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 250
Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
      50              55              60              65

tat cct ctg gtt cca ggg cat gag att gtt ggt gaa gtg acg gaa gta 298
Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
      70              75              80

gga agc aat gta caa aaa ttc aaa gtt gga gac aga gtc ggt gtt gga 346
Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
      85              90              95

tgc att gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 394
Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
      100             105             110

gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 442
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr
      115             120             125

gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gat 490
Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp
      130             135             140             145

gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggt gct 538
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
      150             155             160

gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 586
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr
      165             170             175

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ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc	634
Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly	
180 185 190	
ggg tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag	682
Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys	
195 200 205	
gtt aca gtg att agt aca tcc cct aag aaa gag gag gaa gct cgt aaa	730
Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg Lys	
210 215 220 225	
cac cta gga gct gac tcg ttt ttg gtt agc cgt gac caa gat caa atg	778
His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met	
230 235 240	
cag gct gcc att ggt acc atg gat ggg atc att gac acg gtt tct gca	826
Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala	
245 250 255	
caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag	874
Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys	
260 265 270	
ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctg cca gtt ttt	922
Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe	
275 280 285	
cct tta ctc atg gga aga aag atg gta gct ggt agc ggc att ggg ggt	970
Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly Gly	
290 295 300 305	
atg aag gag aca caa gag atg ata gat ttt gca gcc aag cac aac att	1018
Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn Ile	
310 315 320	
aca gca gac atc gaa gtc ata cca atc gac tac ttg taacactgct	1064
Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu	
325 330	
atggagcgtc tagtcaaagc agatgtcaga taccgttttg tcatcgacat tggaaacaca	1124
ctgaaggcta gctcttaaatt tctgcaatcc agactggatc aatgaagaaa caagaacaga	1184
aacggagact gatttagtgt cataactcggg gttgggttttc cttgtagcat tttttgttgt	1244
ctgctacatg aataatgac acatgaacaa ctgccttctg tgatgatttg ataataaaag	1304
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 <213> Fragaria x ananassa

<220>

<223> Strawberry alcohol acyl transferase

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Ser	Thr	Ser	Ser	Thr	Pro	Leu	Gln	Pro	Tyr	Lys	Leu	Thr	Leu	Leu	Asp
			20				25						30		
Gln	Leu	Thr	Pro	Pro	Ala	Tyr	Val	Pro	Ile	Val	Phe	Phe	Tyr	Pro	Ile
		35					40					45			
Thr	Asp	His	Asp	Phe	Asn	Leu	Pro	Gln	Thr	Leu	Ala	Asp	Leu	Arg	Gln
	50					55					60				
Ala	Leu	Ser	Glu	Thr	Leu	Thr	Leu	Tyr	Tyr	Pro	Leu	Ser	Gly	Arg	Val
65					70					75					80
Lys	Asn	Asn	Leu	Tyr	Ile	Asp	Asp	Phe	Glu	Glu	Gly	Val	Pro	Tyr	Leu
			85						90					95	
Glu	Ala	Arg	Val	Asn	Cys	Asp	Met	Thr	Asp	Phe	Leu	Arg	Leu	Arg	Lys
			100					105					110		
Ile	Glu	Cys	Leu	Asn	Glu	Phe	Val	Pro	Ile	Lys	Pro	Phe	Ser	Met	Glu
		115					120					125			
Ala	Ile	Ser	Asp	Glu	Arg	Tyr	Pro	Leu	Leu	Gly	Val	Gln	Val	Asn	Val
	130					135					140				
Phe	Asp	Ser	Gly	Ile	Ala	Ile	Gly	Val	Ser	Val	Ser	His	Lys	Leu	Ile
145				150					155					160	
Asp	Gly	Gly	Thr	Ala	Asp	Cys	Phe	Leu	Lys	Ser	Trp	Gly	Ala	Val	Phe
			165						170					175	
Arg	Gly	Cys	Arg	Glu	Asn	Ile	Ile	His	Pro	Ser	Leu	Ser	Glu	Ala	Ala
			180					185					190		
Leu	Leu	Phe	Pro	Pro	Arg	Asp	Asp	Leu	Pro	Glu	Lys	Tyr	Val	Asp	Gln
		195				200						205			
Met	Glu	Ala	Leu	Trp	Phe	Ala	Gly	Lys	Lys	Val	Ala	Thr	Arg	Arg	Phe
	210					215					220				
Val	Phe	Gly	Val	Lys	Ala	Ile	Ser	Ser	Ile	Gln	Asp	Glu	Ala	Lys	Ser
225				230						235				240	
Glu	Ser	Val	Pro	Lys	Pro	Ser	Arg	Val	His	Ala	Val	Thr	Gly	Phe	Leu
			245						250					255	
Trp	Lys	His	Leu	Ile	Ala	Ala	Ser	Arg	Ala	Leu	Thr	Ser	Gly	Thr	Thr
		260					265						270		
Ser	Thr	Arg	Leu	Ser	Ile	Ala	Ala	Gln	Ala	Val	Asn	Leu	Arg	Thr	Arg
		275				280					285				

Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp
 290 295 300
 Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser
 305 310 315 320
 Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
 325 330 335
 Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
 340 345 350
 Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
 355 360 365
 Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
 370 375 380
 Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
 385 390 395 400
 Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
 405 410 415
 Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
 420 425 430
 Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro
 435 440 445
 Lys Thr Leu Ile
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 Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu
 1 5 10 15
 gga ggt gtt gga cac atg ggg gtg aag ata gca aag gct atg gga cac 95
 Gly Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His
 20 25 30

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cat atc acc gtg ata agc tct tct gat aag aag aaa aaa gag gcc ttg 143
His Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu
      35              40              45

gag cat att ggt gct gat gag tac ttg gtg agc tct gat gcc acc caa 191
Glu His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln
      50              55              60

atg caa gag gct atg gac tca ctg gat tac att att gac acc att cca 239
Met Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro
      65              70              75

gtg ttc cac cct ctt gag cct tac ctc tct ttg ttg aag ctt gat ggg 287
Val Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly
      80              85              90              95

aag ttg atc ttg atg ggt gtt atc aac acc cca ttg caa ttt gtc tct 335
Lys Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser
      100              105              110

cca ttg gtc atg ctt ggg gag gaa gac gat cac cgg gag ctt tgt ggg 383
Pro Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly
      115              120              125

gag cat gaa gga gat gga gga gat gct cga gtt ctg caa aga gaa aga 431
Glu His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg
      130              135              140

gct gaa acg atg att gaa gtg gtg aag atg gac tac atc aac gaa gct 479
Ala Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala
      145              150              155

ttc gaa agg ttg gag aag aac gac gtt agg tac agg ttc gtt gtg gat 527
Phe Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp
      160              165              170              175

tgt tgc cgg cag caa tct tgatcaataa gaaagaaaga aggcattcatc 575
Cys Cys Arg Gln Gln Ser
      180

gagtggtgtc ctatttttat cgagtactct gtctcatctt atcttaaaca atataaataa 635

acaaagaaaa aaaaaaaaaa aaaaaaaaaa 663

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Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu	
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tgt gaa gac gag ttt aaa aag ata atg aag ata aat ttc atg tct gca	96
Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala	
20 25 30	
tgg ttt ctg gta aat gcc gtt ggc aga aga atg cga gat cat aaa tca	144
Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser	
35 40 45	
gga ggt tcc atc ata ttg ttg acc tcg att gtt gga gct gaa aga ggg	192
Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly	
50 55 60	
ctt tat aca gga gct gtt gcc tat ggt gca tgt tcg gca gca ctg cag	240
Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln	
65 70 75 80	
cag tta gta agg tcg tcg gca ttg gag att gga aaa tac cag atc agg	288
Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg	
85 90 95	
gtt aat gca atc gca cgt ggt ttg cat ttg gaa gat gag ttt cct aag	336
Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys	
100 105 110	
tct gtg gga ata gag aga gca aag aag ctg gtg aat gat gca gtt ccg	384
Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro	
115 120 125	
ctg gag aga tgg ctt gat gtt aaa aat gat gtg gct tca agt gtc ata	432
Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile	
130 135 140	
tat ttg gtc agt gat ggt tca agg tac atg acg ggc aca act ata ttt	480
Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe	
145 150 155 160	
gtt gat ggg gca cag tct ctc gtg agg cct cga atg cgt tct tat atg	528
Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met	
165 170 175	
tgattcttgc tcctattata tcctcctagc cattattagc tacttaggtt tgttcatact	588
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      Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro
            1             5             10

gag att gcg agg agg agg aat gcg cac ttg cag aag cac cct gat gcg    158
Glu Ile Ala Arg Arg Arg Asn Ala His Leu Gln Lys His Pro Asp Ala
            15             20             25

aag ata att cca ctt gga att ggt gat act acc gag cca att cca gaa    206
Lys Ile Ile Pro Leu Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu
            30             35             40

tat ata acc tct gca atg gca aag aga gca ctt gcc atg tcc acc cta    254
Tyr Ile Thr Ser Ala Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu
            45             50             55

gag ggt tac agt ggt tat gga cct gaa caa ggt gaa aag cca ctg aga    302
Glu Gly Tyr Ser Gly Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg
            60             65             70             75

gtt gca att gct aaa acg ttt tat ggc gac ctt ggc ata gag gaa gat    350
Val Ala Ile Ala Lys Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp
            80             85             90

gac ata ttt gtt tct gat ggg gca aaa tgt gac ata tcc cgc ctt cag    398
Asp Ile Phe Val Ser Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln
            95             100             105

gtt ctt ttt ggg gcg gat aaa aca ata gca gtg caa gat cca tcg tat    446
Val Leu Phe Gly Ala Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr
            110             115             120

ccg gct tat gta gac tca agt gtt att atg ggc cag aca gga cag tat    494
Pro Ala Tyr Val Asp Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr
            125             130             135

cag aaa tct gtt cag aag ttt gga aac atc gag tac atg agg tgt act    542
Gln Lys Ser Val Gln Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr
            140             145             150             155

ccc gat aat gga ttt ttt cct gat ctg tcc tct act aag cga aca gat    590
Pro Asp Asn Gly Phe Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp
            160             165             170

atc ata ttt ttc tgt tca cca aac aat cct act ggt tct gct gca aca    638
Ile Ile Phe Phe Cys Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr
            175             180             185

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agg gag caa ctg aca caa ctt gta aag ttt gcc aag gat aat ggt tca	686
Arg Glu Gln Leu Thr Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser	
190 195 200	
atc ata gtc tat gat tct gca tat gcc atg tat atg tca gat gat aat	734
Ile Ile Val Tyr Asp Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn	
205 210 215	
cca cgc tcc atc ttt gaa atc cct gga gct aaa gat gtt gca ctt gag	782
Pro Arg Ser Ile Phe Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu	
220 225 230 235	
aca tca tca ttt agt aag tat gcc gga ttc act gga gtt cgt ttg ggg	830
Thr Ser Ser Phe Ser Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly	
240 245 250	
tgg act gtg gtt cca aag cag ttg cag tat tca gat ggt ttt caa gtt	878
Trp Thr Val Val Pro Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val	
255 260 265	
gcc aag gat ttc aac cgc att gtt tgt act tgc ttc aat ggt gca tcc	926
Ala Lys Asp Phe Asn Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser	
270 275 280	
act att atc caa gct ggt ggt ctg gct tgc ctt caa cca aag ggt gtt	974
Thr Ile Ile Gln Ala Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val	
285 290 295	
aag gct atg cac ggt gtg ata aat ttc tac aaa gaa aat act aag atc	1022
Lys Ala Met His Gly Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile	
300 305 310 315	
ata atg gag acg ttt aac tct ctt ggc ttt aac gtg tat gga ggg aca	1070
Ile Met Glu Thr Phe Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr	
320 325 330	
aac gct cca tat gtg tgg gtc cac ttc cct gga caa agc tcc tgg gat	1118
Asn Ala Pro Tyr Val Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp	
335 340 345	
gtg ttt gct gag atc ctt gag aag act cat gtg gta acc aca cct gga	1166
Val Phe Ala Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly	
350 355 360	
agt ggc ttt gga cct ggt ggt gaa ggt ttc atc agg gta agt gcc ttt	1214
Ser Gly Phe Gly Pro Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe	
365 370 375	
gga cac agg aaa aat ata tta gaa gca tgt aaa aga ttc aag caa tta	1262
Gly His Arg Lys Asn Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu	
380 385 390 395	
tac aag tgaggactgc ggatctgaat tgtagaccag tttctactgc atgctagttg	1318
Tyr Lys	
aacctatttg cctcccattt ccgttctatg ctaaataattt tagcacgttc caattccgta	1378

ttcagtttgt cggcttttagt ttatgaatta tggagatttt agctattgta aaaatgattc 1438
gatcagcctt gttttcatgt gttacactta attgttgtaa catttgtagag gatcagaagc 1498
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Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
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cca gca aat cct aca ccc tat gaa ttt aaa caa ctt tct gat gtg gat 96
Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
20 25 30

gat caa caa agc tta agg ctt caa ttg cca ttc gta aat atc tat ccc 144
Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
35 40 45

cat aat cca agt ttg gag gga aga gat cca gtg aag gta ata aag gaa 192
His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
50 55 60

gca att gga aag gcg ttg gtg ttc tac tat cct tta gca gga aga ttg 240
Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
65 70 75 80

aga gaa ggg cca ggt aga aag ctt ttt gtt gaa tgt aca ggt gaa gga 288
Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
85 90 95

atc ttg ttt att gaa gcg gat gca gat gtg agc tta gaa gaa ttt tgg 336
Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
100 105 110

gat act ctt cca tat tca ctt tca agc atg cag aac aat att ata cat 384
Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
115 120 125

aac gct tta aat tct gat gaa gtc ctc aat tct cca tta ttg ctc att 432
Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile

130	135	140	
cag gtg aca cga ctc aag tgt gga ggt ttc att ttt ggt ctt tgt ttc			480
Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe			
145	150	155	160
aat cat act atg gca gat ggt ttt ggt att gtc caa ttc atg aag gct			528
Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala			
	165	170	175
aca gcg gag ata gct cgt gga gct ttt gct cca tct att tta cca gta			576
Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val			
	180	185	190
tgg caa aga gct ctc tta acc gca aga gac cct ccc aga atc act ttt			624
Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe			
	195	200	205
cgc cac tat gaa tac gac caa gta gtc gac atg aag agc ggc ctc att			672
Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile			
	210	215	220
cca gtc aat agc aag atc gat caa tta ttc ttc ttt agc caa ctt caa			720
Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln			
225	230	235	240
atc tcc acc ctt cgc caa act ttg cca gcc cac ctt cac gat tgc cct			768
Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro			
	245	250	255
tcc ttc gag gtc ctc act gcc tat gtt tgg cgc ctc cgt acc ata gcc			816
Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala			
	260	265	270
ctt caa ttt aag cca gag gag gaa gtg cgg ttt ctt tgc gta atg aat			864
Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn			
	275	280	285
cta cgc tcg aag atc gac ata cca tta ggg tat tat ggt aat gcg gta			912
Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val			
	290	295	300
gtt gtt cct gca gta atc acc acc gct gcg aag ctt tgt ggg aac cca			960
Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro			
305	310	315	320
ctt ggt tat gct gta gac ttg att agg aag gcc aag gct aag gca acg			1008
Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr			
	325	330	335
atg gag tac ata aag tct acg gtg gat ctt atg gtg att aaa gga cga			1056
Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg			
	340	345	350
ccc tat ttc act gta gtt gga tca ttt atg atg tca gac cta acg aga			1104
Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg			
	355	360	365

att ggg gtt gaa aac gtg gac ttt gga tgg gga aag gcc att ttt gga 1152
 Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly
 370 375 380

gga cct aca acc aca ggg gcc aga att aca cga ggt ttg gta agc ttt 1200
 Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe
 385 390 395 400

tgt gta cct ttc atg aat aga aat gga gaa aag gga act gcg tta agt 1248
 Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser
 405 410 415

cta tgc ttg cct cct cca gcc atg gaa aga ttt agg gca aat gtt cat 1296
 Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His
 420 425 430

gcc tcg ttg caa gtg aaa caa gtg gtt gat gca gtt gat agc cat atg 1344
 Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met
 435 440 445

caa act att caa tct gct tcg aaa taaataatat tgttgaaggt gggctctgagt 1398
 Gln Thr Ile Gln Ser Ala Ser Lys
 450 455

tgactcgacc atatcgatgc atgcaagctt gatccggctg ctaacaaagc ccgaaaggaa 1458

gctgagttgc tgt 1471

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 <213> Malus sp.

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 <223> cDNA

<220>
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<220>
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 <223> N is any nucleic acid

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 1 5 10 15

act ccg gca aag tca acg cct caa gaa aca aag ttt ctc tca gat att 96
 Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
 20 25 30

gac gac caa gaa agc ttg aga gtt cag att cca atc ata atg tgt tac 144

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr	
35 40 45	
aaa gac aac cct tca ctt aat aaa aat cgt aat ccc gtt aag gca att	192
Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile	
50 55 60	
agg gaa gcc tta agt aga gca tta gtg tat tac tac ccc tta gct gga	240
Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly	
65 70 75 80	
agg ctt agg gaa ggg cct aat aga aag ctc gtg gtc gat tgc aat ggt	288
Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly	
85 90 95	
gaa ggt atc ttg ttc gtt gag gct tct gct gat gtc aca ctt gag caa	336
Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln	
100 105 110	
cta gga gac aaa att cta ccc cct tgt cca ctt tta gag gag ttc tta	384
Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu	
115 120 125	
tat aat ttt cca ggc tct gat gga att att gat tgt cct ttg ctg ctg	432
Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu	
130 135 140	
att cag gtg acc tgt ctt aca tgt gga ggt ttc ata ctt gca ttg cgc	480
Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg	
145 150 155 160	
cta aac cac aca atg tgt gat gca gct gga ttg ctc ttg ttc ctg acc	528
Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr	
165 170 175	
gcc atc gcg gag atg gca aga ggc gca cat gca cca tct att cta cca	576
Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro	
180 185 190	
gtg tgg gag aga gag ctc ttg ttc gct cga gat cca cca aga att aca	624
Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr	
195 200 205	
tgt gct cgt cat gaa tat gaa gac gtg att ggt cat tct gat ggc tca	672
Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser	
210 215 220	
tac gca tcc agt aac cag tca aac atg gtt caa cga tct ttc tac ttt	720
Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe	
225 230 235 240	
ggg gcc aag gag atg aga gtc ctt cga aaa cag att cca ccc cac cta	768
Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu	
245 250 255	
att tcc act tgc tcc aca ttt gac ttg atc aca gct tgt ttg tgg aaa	816
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys	

260	265	270	
tgt cgc act ctt gca ctt aac att aat cca aaa gag gct gtt cga gtt			864
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val			
275	280	285	
tca tgc att gtc aat gca cga gga aag cac aac aat gta cgt ctt ccc			912
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro			
290	295	300	
ttg gga tac tat ggc aat gca ttt gca ttt cca gct gca att tcg aag			960
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys			
305	310	315	320
gct gaa cct cta tgc aaa aat cca ctg gga tat gct ttg gag ttg gtg			1008
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val			
325	330	335	
aag aag gct aaa gct acc atg aat gaa gaa tac tta aga tca gtg gca			1056
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala			
340	345	350	
gat ctt ttg gta cta aga ggg cga cct caa tat tca tcg aca gga agt			1104
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser			
355	360	365	
tat tta ata gtt tct gat aat acg cgt gta ggt ttt gga gat gtc aat			1152
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn			
370	375	380	
ttt gga tgg gga cag ccg gta ttt gct gga ccc gtc aag gcc ttg gat			1200
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp			
385	390	395	400
ttg att agc ttc tac gtt caa cac aaa aac aac aca gag gat gga ata			1248
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile			
405	410	415	
ttg gta cca atg tgt ttg cca tcc tcg gcc atg gag aga ttt cag cag			1296
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln			
420	425	430	
gaa cta gag agg att act cag gaa cct aag gag gat ata tgt aac aac			1344
Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn			
435	440	445	
ctt aga tca act agt caa tgatgtaagt gttaaacgta atgcactttc			1392
Leu Arg Ser Thr Ser Gln			
450			
tgtaatgtag agttgtgtct cttggaactt atcncaagag ttatagctgt tatccaaagg			1452
tctgaatggt attaaaaaat agccaataat aag			1485

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 <213> Musa sp.

<220>
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 <223> cDNA

<220>
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ggg gtc acg ccg acg ggc tcg ctc ggc ctc tcc gcc atc gac cgg gtg 96
Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
             20             25             30

ccc ggc ctc agg cat atg gtg cgg tcg cta cac gtg ttc agg caa ggc 144
Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
             35             40             45

cgg gag ccg gcc agg atc atc agg gaa gca ctg tcg aag gcg ctg gtg 192
Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
             50             55             60

aag tac tac ccc ttc gcg ggg cgg ttc gtg gac gat ccc gag ggc ggc 240
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
             65             70             75             80

ggc gag gtt cgt gtc gct tgc act ggc gag ggc gct tgg ttc gtc gag 288
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
             85             90             95

gcc aag gcg gac tgc agc ttg gag gac gtg aag tac ctc gat ctc ccg 336
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
             100            105            110

ctc atg atc cct gag gac gcg ctc ctg ccc aag ccc tgc ccg gga ctg 384
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
             115            120            125

aac ccc ctc gac ctc cct ctc atg ctg cag gtg aca gag ttc gtg ggc 432
Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
             130            135            140

ggc gga ttc gtg gtc ggc ctc atc tcc gtc cat acc atc gcc gac ggc 480
Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
             145            150            155            160

ctc ggc gtc gtc cag ttc atc aac gcc gtc gcc gag atc gcc cgt ggc 528
Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
             165            170            175

ctg ccg aag ccc acc gtg gag cct gca tgg tcc cgg gag gtc ata ccc 576
Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
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aac cca cct aag ctg cct ccc ggt ggc ccg ccc gtg ttc ccc tcc ttc	624
Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe	
195 200 205	
aag ctg ctc cac gcc acc gtc gac cta tcc cct gac cac atc gat cac	672
Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His	
210 215 220	
gtc aag tcc cga cac ttg gag ctc acc ggc cag cgc tgc tct acc ttc	720
Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe	
225 230 235 240	
gac gtc gcc atc gcc aac ctg tgg cag tcc cgc acg cgc gcc atc aac	768
Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn	
245 250 255	
ctg gac cca ggc gtc gac gtg cac gtg tgc ttc ttc gcc aac act cgc	816
Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg	
260 265 270	
cac ctg ttg cgc cag gtc gtc ctc ctg ccc ccc gag gat ggc tac tac	864
His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr	
275 280 285	
ggc aac tgc ttc tac ccg gtg acc gcc acc gcc cca agc ggc agg atc	912
Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile	
290 295 300	
gca tcg gcc gag ctc atc gat gtc gtc agc atc atc agg gac gcc aag	960
Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys	
305 310 315 320	
tcg agg ctg ccg ggc gag ttc gcc aag tgg gct gcc ggg gat ttc aag	1008
Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys	
325 330 335	
gac gac cct tac gag ctc agc ttc acg tac aac tcg ctg ttc gtg tcg	1056
Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser	
340 345 350	
gac tgg acc cgg ctc ggc ttc ctc gac gtc gac tac ggc tgg ggc aag	1104
Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys	
355 360 365	
ccc ctc cac gtt ata ccg ttc gcg tac ttg gac atc atg gcg gtc ggc	1152
Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly	
370 375 380	
atc atc ggg gcg ccg ccg gcg ccg caa aag ggg act cgg gtg atg gcg	1200
Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala	
385 390 395 400	
cag tgc gtc gag aag gag cac atg cag gcg ttc ctg gaa gag atg aaa	1248
Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys	
405 410 415	
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Gly Phe Ala

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<220>
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 <223> cDNA

<220>
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 1 5 10 15

tca act tcc tct tca cca ctt cag cct tac aag ctt acc ctg ctc gac 96
 Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
 20 25 30

cag ctc act cct cca tcg tat gtc ccc atg gta ttc ttc tac ccc att 144
 Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
 35 40 45

act ggc cct gca gtc ttc aat ctt caa acc cta gct gac tta aga cat 192
 Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His
 50 55 60

gcc ctt tcc gag act ctc act ttg tac tat cca ctc tct gga agg gtc 240
 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
 65 70 75 80

aaa aac aac cta tac atc gat gat ttt gaa gag ggt gtc cca tac ctt 288
 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
 85 90 95

gag gct cga gtg aac tgt gac atg aat gat ttt cta agg ctt ccg aaa 336
 Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys
 100 105 110

atc gag tgc cta aat gag ttt gtt cca ata aaa cca ttt agt atg gaa 384
 Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
 115 120 125

gca ata tct gat gag cgt tac cct ttg ctc gga gtt caa gtt aac att 432
 Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile
 130 135 140

ttc aac tcc gga ata gca atc ggg gtc tcc gtc tct cac aag ctc atc 480
 Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
 145 150 155 160

gat gga aga act tca gac tgt ttt ctc aag tcg tgg tgt gct gtt ttt 528
 Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe

165										170					175					
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Arg	Gly	Ser	Arg	Asp	Lys	Ile	Ile	His	Pro	Asn	Leu	Ser	Gln	Ala	Ala					
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Leu	Leu	Phe	Pro	Pro	Arg	Asp	Asp	Leu	Pro	Glu	Lys	Tyr	Ala	Arg	Gln					
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Met	Glu	Gly	Leu	Trp	Phe	Val	Gly	Lys	Lys	Val	Ala	Thr	Arg	Arg	Phe					
			210				215				220									
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225				230				235				240								
gag	tcc	gtg	ccc	aag	cca	tca	cga	gtt	cag	gct	gtc	act	agt	ttt	ctc	768				
Glu	Ser	Val	Pro	Lys	Pro	Ser	Arg	Val	Gln	Ala	Val	Thr	Ser	Phe	Leu					
			245				250				255									
tgg	aaa	cat	cta	atc	gct	act	tct	cgg	gca	cta	aca	tca	ggt	act	act	816				
Trp	Lys	His	Leu	Ile	Ala	Thr	Ser	Arg	Ala	Leu	Thr	Ser	Gly	Thr	Thr					
			260				265				270									
tca	aca	aga	ctt	tct	ata	gca	acc	cag	gta	gtg	aac	ata	aga	tca	cgg	864				
Ser	Thr	Arg	Leu	Ser	Ile	Ala	Thr	Gln	Val	Val	Asn	Ile	Arg	Ser	Arg					
			275				280				285									
agg	aac	atg	gag	aca	gtg	tgg	gat	aat	gcc	att	gga	aac	ttg	ata	tgg	912				
Arg	Asn	Met	Glu	Thr	Val	Trp	Asp	Asn	Ala	Ile	Gly	Asn	Leu	Ile	Trp					
			290				295				300									
ttc	gct	ccg	gcc	ata	cta	gag	cta	agt	cat	aca	aca	cta	gag	atc	agt	960				
Phe	Ala	Pro	Ala	Ile	Leu	Glu	Leu	Ser	His	Thr	Thr	Leu	Glu	Ile	Ser					
305				310				315				320								
gat	ctt	aag	ctg	tgt	gac	ttg	gtt	aac	ttg	ctc	aat	gga	tct	gtc	aaa	1008				
Asp	Leu	Lys	Leu	Cys	Asp	Leu	Val	Asn	Leu	Leu	Asn	Gly	Ser	Val	Lys					
			325				330				335									
caa	tgt	aac	ggt	gat	tac	ttt	gag	act	ttc	atg	ggt	aaa	gag	gga	tat	1056				
Gln	Cys	Asn	Gly	Asp	Tyr	Phe	Glu	Thr	Phe	Met	Gly	Lys	Glu	Gly	Tyr					
			340				345				350									
gga	agc	atg	tgc	gag	tat	cta	gat	ttt	cag	agg	act	atg	agt	tct	atg	1104				
Gly	Ser	Met	Cys	Glu	Tyr	Leu	Asp	Phe	Gln	Arg	Thr	Met	Ser	Ser	Met					
			355				360				365									
gaa	cca	gca	cca	gag	att	tat	tta	ttc	acg	agc	tgg	act	aat	ttt	ttc	1152				
Glu	Pro	Ala	Pro	Glu	Ile	Tyr	Leu	Phe	Thr	Ser	Trp	Thr	Asn	Phe	Phe					
			370				375				380									
aac	caa	ctt	gat	ttt	gga	tgg	ggg	agg	aca	tca	tgg	att	gga	gtt	gca	1200				
Asn	Gln	Leu	Asp	Phe	Gly	Trp	Gly	Arg	Thr	Ser	Trp	Ile	Gly	Val	Ala					
385				390				395				400								

gga aaa att gaa tct gca ttt tgc aat ctc aca aca tta gtt cca aca 1248
 Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
 405 410 415

cca tgc gat act gga att gaa gcg tgg gtg aat cta gaa gaa gaa aaa 1296
 Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
 420 425 430

atg gct atg cta gaa caa gat ccc cag ttt cta gca cta gca tct cca 1344
 Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
 435 440 445

aag acg cta att tca aga tat tgattaagga agattatgcg gctcgtgcaa 1395
 Lys Thr Leu Ile Ser Arg Tyr
 450 455

tgtttccatt ttgttgtgat taaggcttaa attagttcac cagccaatca ataagatgca 1455

agtatgatag actcgggtcta cgtatgttat ccg 1488

<210> 14
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 <213> Citrus limon

<220>
 <223> Citrus limon alcohol acyl transferase

<400> 14
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 1 5 10 15
 Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val Pro
 20 25 30
 Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp Cys
 35 40 45
 Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Lys Ala Leu Ser Glu Val
 50 55 60
 Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu Asn
 65 70 75 80
 Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu Glu
 85 90 95
 Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln Gly
 100 105 110
 Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp Ile
 115 120 125
 Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys Gly
 130 135 140

Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly Ala
 145 150 155 160
 Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly Val
 165 170 175
 Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val Gly
 180 185 190
 Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro Pro
 195 200 205
 Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr Ala
 210 215 220
 Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys Ser
 225 230 235 240
 Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile Leu
 245 250 255
 Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser Asp
 260 265 270
 Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg Leu
 275 280 285
 Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Thr
 290 295 300
 Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn His
 305 310 315 320
 Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu Tyr
 325 330 335
 Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn Ala
 340 345 350
 Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile Val
 355 360 365
 Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly Gln
 370 375 380
 Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala His
 385 390 395 400
 Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile Asn
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Phe Asp

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<211> 1296

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 <213> Mangifera indica

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<220>
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acg ccg agg ata tct ctg tgg aac tcc aac gcc gat ctg gtg gtt ccc	96
Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro	
20 25 30	
cga ttt cat act ccc agc gtt tac ttc tac cgg ccc acc ggg gcc ata	144
Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile	
35 40 45	
aac ttc ttt gat ggt aag ttg ctc aag gag gct ctc ggc aag gct ctg	192
Asn Phe Phe Asp Gly Lys Leu Lys Glu Ala Leu Gly Lys Ala Leu	
50 55 60	
gtg ccg ttc tac cca atg gcg ggg cgg tta aag cgt gac gaa gat gga	240
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly	
65 70 75 80	
agg att gag atc gat tgt aat gct gaa ggc gtc ttg ttt gtt gag gcc	288
Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala	
85 90 95	
gaa act ccc tct gtt att gat gat ttt ggt gac ttt gcg ccc act tta	336
Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu	
100 105 110	
gag ctc aag cag ctc att ccg aca gtg gat tac tcc ggc ggg atc tct	384
Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser	
115 120 125	
acg tat ccc cta ttg gcg tta cag gtt act cac ttc aaa tgt ggt gga	432
Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly	
130 135 140	
gtt tca ctt ggt gta ggt atg caa cac cat gcg gca gat gga ttt tct	480
Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser	
145 150 155 160	
ggg ctt cac ttt gta aac aca tgg tca gac att gct cgt ggt ctt gat	528
Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp	
165 170 175	
gtt aac atc acc ctg ttc att gac cgg act ctg ctc aga gca cag gat	576

Val	Asn	Ile	Thr	Leu	Phe	Ile	Asp	Arg	Thr	Leu	Leu	Arg	Ala	Gln	Asp	
			180					185					190			
ccc	cct	cag	cct	act	ttc	cca	cac	aca	tgg	aat	acc	agg	ccg	cct	cct	624
Pro	Pro	Gln	Pro	Thr	Phe	Pro	His	Thr	Trp	Asn	Thr	Arg	Pro	Pro	Pro	
		195					200				205					
tcc	ctg	aaa	act	cct	cca	cca	gca	gtt	tct	gag	cct	act	gct	gtc	tcc	672
Ser	Leu	Lys	Thr	Pro	Pro	Pro	Ala	Val	Ser	Glu	Pro	Thr	Ala	Val	Ser	
	210					215					220					
att	ttt	aag	ttg	acg	cgg	gac	cag	ctc	aac	atc	ctc	aaa	gcc	aag	gcc	720
Ile	Phe	Lys	Leu	Thr	Arg	Asp	Gln	Leu	Asn	Ile	Leu	Lys	Ala	Lys	Ala	
225					230				235					240		
aaa	gaa	gat	ggg	aac	act	atc	aac	tat	agc	tca	tat	gag	atg	ctg	gcg	768
Lys	Glu	Asp	Gly	Asn	Thr	Ile	Asn	Tyr	Ser	Ser	Tyr	Glu	Met	Leu	Ala	
				245				250						255		
ggg	cat	gtc	tgg	aga	tct	gca	tgc	aag	gca	cgc	ggc	tta	tct	gat	gat	816
Gly	His	Val	Trp	Arg	Ser	Ala	Cys	Lys	Ala	Arg	Gly	Leu	Ser	Asp	Asp	
		260						265				270				
caa	gag	act	aaa	ttg	tac	ata	gca	act	gac	gga	cgt	gct	aga	tta	atc	864
Gln	Glu	Thr	Lys	Leu	Tyr	Ile	Ala	Thr	Asp	Gly	Arg	Ala	Arg	Leu	Ile	
		275					280					285				
ccc	cca	ctt	cca	cct	ggg	tac	ttt	ggg	aat	gtg	ata	ttt	aca	gcc	aca	912
Pro	Pro	Leu	Pro	Pro	Gly	Tyr	Phe	Gly	Asn	Val	Ile	Phe	Thr	Ala	Thr	
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cca	atg	gca	gta	gca	ggg	gat	ctc	cag	tca	aag	cct	ata	tgg	tat	gct	960
Pro	Met	Ala	Val	Ala	Gly	Asp	Leu	Gln	Ser	Lys	Pro	Ile	Trp	Tyr	Ala	
305					310					315					320	
gct	ggc	cag	att	cat	gat	gcc	ttg	gtt	cga	atg	gac	aac	gac	tat	tta	1008
Ala	Gly	Gln	Ile	His	Asp	Ala	Leu	Val	Arg	Met	Asp	Asn	Asp	Tyr	Leu	
			325						330					335		
agg	tca	gcc	ctc	gat	tac	cta	gag	ctt	cag	cct	gat	tta	tca	gca	tta	1056
Arg	Ser	Ala	Leu	Asp	Tyr	Leu	Glu	Leu	Gln	Pro	Asp	Leu	Ser	Ala	Leu	
		340						345				350				
gtt	cgt	ggg	gcc	cat	aca	ttt	agg	tgt	cca	aat	ctc	ggg	att	act	agt	1104
Val	Arg	Gly	Ala	His	Thr	Phe	Arg	Cys	Pro	Asn	Leu	Gly	Ile	Thr	Ser	
		355					360					365				
tgg	gtt	aga	ctg	cca	ata	cat	gat	gca	gat	ttt	ggg	tgg	ggg	cca	ccc	1152
Trp	Val	Arg	Leu	Pro	Ile	His	Asp	Ala	Asp	Phe	Gly	Trp	Gly	Pro	Pro	
	370					375					380					
aca	ttt	atg	ggg	cct	ggg	ggg	att	gca	tat	gaa	ggc	tta	tca	ttt	gta	1200
Thr	Phe	Met	Gly	Pro	Gly	Gly	Ile	Ala	Tyr	Glu	Gly	Leu	Ser	Phe	Val	
385					390					395					400	
ttg	cca	agc	cct	aca	aat	gat	ggg	agc	tta	tca	gtt	gcc	atc	tct	cta	1248
Leu	Pro	Ser	Pro	Thr	Asn	Asp	Gly	Ser	Leu	Ser	Val	Ala	Ile	Ser	Leu	
				405					410					415		

caa tct gaa cac atg aaa ctg ttt cag aag ttc ttt tat gat att taa 1296
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 <213> Citrus limon

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<220>
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 1 5

acc gaa atc atc aag cct tct tcg ccg acg cct caa cac caa agt acc 102
 Thr Glu Ile Ile Lys Pro Ser Ser Pro Thr Pro Gln His Gln Ser Thr
 10 15 20

tat aaa ctt tca att att gat caa tta act cct aat gtt tac ttt tcc 150
 Tyr Lys Leu Ser Ile Ile Asp Gln Leu Thr Pro Asn Val Tyr Phe Ser
 25 30 35

atc att ctc ttg tat tca aaa gct ggt gaa agt acc gcc aaa act tca 198
 Ile Ile Leu Leu Tyr Ser Lys Ala Gly Glu Ser Thr Ala Lys Thr Ser
 40 45 50 55

gat cac ctc aaa gaa tct ctt tca aat aca tta acc cac tac tat cct 246
 Asp His Leu Lys Glu Ser Leu Ser Asn Thr Leu Thr His Tyr Tyr Pro
 60 65 70

tta gct ggg caa ctc aaa tat gat caa ctt att gtt gat tgt aac gac 294
 Leu Ala Gly Gln Leu Lys Tyr Asp Gln Leu Ile Val Asp Cys Asn Asp
 75 80 85

caa ggt gtc ccg ttc atc gaa gca cac gtc acc aac gac atg cgt cag 342
 Gln Gly Val Pro Phe Ile Glu Ala His Val Thr Asn Asp Met Arg Gln
 90 95 100

ctt ctt aaa ata cca aat att gat gtt ctc gaa caa ctc cta cca ttc 390
 Leu Leu Lys Ile Pro Asn Ile Asp Val Leu Glu Gln Leu Leu Pro Phe
 105 110 115

aaa ccg cat gag ggt ttt gat tct gat cgt tcc aac cta acc gtt cag 438
 Lys Pro His Glu Gly Phe Asp Ser Asp Arg Ser Asn Leu Thr Val Gln
 120 125 130 135

gtc aat tac ttt ggt tgt gaa gga atg gcg att ggt ctg tgc ttc aga 486
 Val Asn Tyr Phe Gly Cys Glu Gly Met Ala Ile Gly Leu Cys Phe Arg

140	145	150	
cac aaa gtt att gat gca aca acg gct gca ttc ttt gtt aag aac tgg			534
His Lys Val Ile Asp Ala Thr Thr Ala Ala Phe Phe Val Lys Asn Trp			
155	160	165	
ggt gta att gct cgt ggt gct gga gaa att aag gac gtg atc att gat			582
Gly Val Ile Ala Arg Gly Ala Gly Glu Ile Lys Asp Val Ile Ile Asp			
170	175	180	
cat gct tcc ctg ttt ccc gca aga gat tta tct tgc tta aca aag agt			630
His Ala Ser Leu Phe Pro Ala Arg Asp Leu Ser Cys Leu Thr Lys Ser			
185	190	195	
ggt gac gaa gag ttt ttg aag cca gag tct gaa aca aag cgc ttt gtg			678
Val Asp Glu Glu Phe Leu Lys Pro Glu Ser Glu Thr Lys Arg Phe Val			
200	205	210	215
ttt gat ggt gcc act ata gct tct tta caa gaa acg ttt gca agt ttt			726
Phe Asp Gly Ala Thr Ile Ala Ser Leu Gln Glu Thr Phe Ala Ser Phe			
220	225	230	
gaa cga cgt cca aca cgc ttt gag gtt gtg tca gca gtt att ttg ggt			774
Glu Arg Arg Pro Thr Arg Phe Glu Val Val Ser Ala Val Ile Leu Gly			
235	240	245	
gct ttg ata act gca acg aga gaa tct gat gat gag tct aac gtt cct			822
Ala Leu Ile Thr Ala Thr Arg Glu Ser Asp Asp Glu Ser Asn Val Pro			
250	255	260	
gaa cgt ttg gac acg ata att tca gtg aat cta cgg cag aga atg aat			870
Glu Arg Leu Asp Thr Ile Ile Ser Val Asn Leu Arg Gln Arg Met Asn			
265	270	275	
cca cca ttc ccg gag cat tgc atg ggg aat ata ata tcc ggg gga tta			918
Pro Pro Phe Pro Glu His Cys Met Gly Asn Ile Ile Ser Gly Gly Leu			
280	285	290	295
gtg tat tgg cca ctg gag aaa aaa gtt gat tac ggg tgt tta gca aaa			966
Val Tyr Trp Pro Leu Glu Lys Lys Val Asp Tyr Gly Cys Leu Ala Lys			
300	305	310	
gag att cat gaa tca ata aag aaa gtg gac gat caa ttt gcg agg aag			1014
Glu Ile His Glu Ser Ile Lys Lys Val Asp Asp Gln Phe Ala Arg Lys			
315	320	325	
ttc tat ggg gac gca gag ttc ttg aac ctg ccg agg ctt gcg ggt gct			1062
Phe Tyr Gly Asp Ala Glu Phe Leu Asn Leu Pro Arg Leu Ala Gly Ala			
330	335	340	
gag gat gtg aag aag cgg gag ttt tgg gtt act agt tgg tgc aaa act			1110
Glu Asp Val Lys Lys Arg Glu Phe Trp Val Thr Ser Trp Cys Lys Thr			
345	350	355	
ccg ctg tat gaa gct gat ttc ggg tgg ggg aat cct aag tgg gca ggc			1158
Pro Leu Tyr Glu Ala Asp Phe Gly Trp Gly Asn Pro Lys Trp Ala Gly			
360	365	370	375

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aac tcc atg agg ctt aat cag att act gtt ttc ttt gac agt agt gat 1206
Asn Ser Met Arg Leu Asn Gln Ile Thr Val Phe Phe Asp Ser Ser Asp
          380          385          390

ggt gag gga gtt gaa gct tgg gtg ggg ttg ccc aga aaa gac atg gct 1254
Gly Glu Gly Val Glu Ala Trp Val Gly Leu Pro Arg Lys Asp Met Ala
          395          400          405

cga ttt gaa aaa gat tct ggc atc ctt gct tac act tcc cct aat cca 1302
Arg Phe Glu Lys Asp Ser Gly Ile Leu Ala Tyr Thr Ser Pro Asn Pro
          410          415          420

agc ata ttt tgagggttta tttatttttt attgcactgt ttgttatttg 1351
Ser Ile Phe
          425

tactggcttg ctgggaacat attctggcaa atttcgctga tgcaagtatc attctccata 1411

aaaatgtcaa aaaaaaaaaa aaaaaa 1436

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<213> Citrus limon

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<223> cDNA

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                                   Met Ala
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gca att gaa aac aga gta aca cta aag aag cat gag gtt acc aaa gtc 105
Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr Lys Val
          5          10          15

acc cct ttc gtc aac ccc aac tca aag acg acg tcg ttt act ctc gat 153
Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr Leu Asp
          20          25          30

ctc acc tat ttc gac ttt ttc tgg ttc aag aat cct cct gtg gaa cgc 201
Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val Glu Arg
          35          40          45          50

ctc ttc ttc tat gag atg act gac ttg acg tgg gat tta ttc aac tcg 249
Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe Asn Ser
          55          60          65

gag atc ctc cca aag ctg aag cac tcc ctt tcc ttc act ctc ctt cat 297

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Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu Leu His	
70 75 80	
tac ctc cct ctt gct ggt cac atc atg tgg ccg ctg gat gcc gca aag	345
Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala Ala Lys	
85 90 95	
cct gcc gtc tac tac ttt ccc gac caa aac gac ggc gtt tca ttc gca	393
Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser Phe Ala	
100 105 110	
gtt gct gag tgg tct tcc gag tgc cac gca ggc ttc cat cac ctc tcc	441
Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His Leu Ser	
115 120 125 130	
ggc aac gga atc cgc caa gca gtt gaa ttt cat cct ctt gtg ccc cag	489
Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val Pro Gln	
135 140 145	
ttg tcg ctt acg gac gat aaa gct gag gta att gcc atc caa ata aca	537
Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln Ile Thr	
150 155 160	
ctg ttt ccg aat caa ggc ttc tca att ggt gtt tca tct cac cat gca	585
Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His His Ala	
165 170 175	
att ctt gat gga aaa act tcg acc ttg ttc ctg aaa tct tgg gct tat	633
Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp Ala Tyr	
180 185 190	
ttg tgc aaa caa tta caa tta tgc cat cac cct tgt ttg tca cct gaa	681
Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser Pro Glu	
195 200 205 210	
cta acc cct ctt ctc gac cgg act gtc atc aaa gat ccg aca ggt cag	729
Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr Gly Gln	
215 220 225	
gac atg ctg caa ctg aat aag tgg gtt gtc ggg tcg gat aat tcg gat	777
Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn Ser Asp	
230 235 240	
ccc cag aag ata cgg agc ttg aag gtt tta cca ttc tta gac tct gag	825
Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp Ser Glu	
245 250 255	
tct ctg aac aaa ttg gtc cga gcc aca ttt gag ttg acg cgt gaa gat	873
Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg Glu Asp	
260 265 270	
att acg aaa ctc agg cac aag gtt aat cat cag tta tca aaa tca tca	921
Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys Ser Ser	
275 280 285 290	
aaa tca aag caa gtt cgt tta tca act ttt gtg ctt aca tta gct tat	969
Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu Ala Tyr	

295	300	305	
gtg ttt gtt tgc atg gct aaa gct	aaa tta gcc aaa gcc aaa act gaa		1017
Val Phe Val Cys Met Ala Lys Ala	Lys Leu Ala Lys Ala Lys Thr Glu		
310	315	320	
gct gaa gct gca gca ggt aat gat	gaa att aaa aat att att gtg gga		1065
Ala Glu Ala Ala Ala Gly Asn Asp	Glu Ile Lys Asn Ile Ile Val Gly		
325	330	335	
ttc act gcg gat tat agg agc cgt	ttg gat cct cca att cca ctt aat		1113
Phe Thr Ala Asp Tyr Arg Ser Arg	Leu Asp Pro Pro Ile Pro Leu Asn		
340	345	350	
tat ttt ggt aac tgc aat ggg aga	cat tgt gag act gca aaa gca agt		1161
Tyr Phe Gly Asn Cys Asn Gly Arg	His Cys Glu Thr Ala Lys Ala Ser		
355	360	365	370
gat ttc gtt caa gaa aat ggg gtt	gct ttt gtt gca gag atg tta agt		1209
Asp Phe Val Gln Glu Asn Gly Val	Ala Phe Val Ala Glu Met Leu Ser		
375	380	385	
gat atg gtc aaa ggg atc gat gcg	gat gcc att gaa gcc aat gat gat		1257
Asp Met Val Lys Gly Ile Asp Ala	Asp Ala Ile Glu Ala Asn Asp Asp		
390	395	400	
aag gtt tca gaa ata ttg gaa att	ctg aaa gaa gga gca atg att ttt		1305
Lys Val Ser Glu Ile Leu Glu Ile	Leu Lys Glu Gly Ala Met Ile Phe		
405	410	415	
tct gtg gct ggc tcg acc caa ttt	gat gtt tac ggg tcg gat ttc ggg		1353
Ser Val Ala Gly Ser Thr Gln Phe	Asp Val Tyr Gly Ser Asp Phe Gly		
420	425	430	
tgg ggg agg ccc aag aag gtg gag	att gtg tca ata gat agg aca caa		1401
Trp Gly Arg Pro Lys Lys Val Glu	Ile Val Ser Ile Asp Arg Thr Gln		
435	440	445	450
gcc atc tct ttg gca gag aga aga	gat gga gga ggc ggc gtt gag gtt		1449
Ala Ile Ser Leu Ala Glu Arg Arg	Asp Gly Gly Gly Gly Val Glu Val		
455	460	465	
gga gtt gtt tta gag aag caa caa	atg gag gtt ttt gaa tct gta ttt		1497
Gly Val Val Leu Glu Lys Gln Gln	Met Glu Val Phe Glu Ser Val Phe		
470	475	480	
gct gat gga ctg aaa aat gat ctt	ggt taattaatga tgtatcatct		1544
Ala Asp Gly Leu Lys Asn Asp Leu	Val		
485	490		
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 <213> Citrus limon

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<220>
 <223> Lemon acyl transferase

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 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr
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 Pro Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp
 20 25 30
 tct cag ctt ttc ttg cgt ttc act att gag tat ctc ttg gtc tat aga 144
 Ser Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg
 35 40 45
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 Pro Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser
 50 55 60
 gca ctc gcc aaa gcc ttg gtt cct tac tat ccc ctc gcg ggt cgg gtc 240
 Ala Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val
 65 70 75
 aga gct aaa caa gac ggg tcg ggc tta ttg gaa gtc gtg tgt cta ggc 288
 Arg Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly
 80 85 90 95
 caa ggc gct gtg ttc atc gaa gcc gtc gac cgt gaa agt acg atc acc 336
 Gln Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr
 100 105 110
 gat ttt gag agt gct ccc agg tat gtt act cag tgg agg aaa ctg ctg 384
 Asp Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu
 115 120 125
 tcg tta tac gtg gcg gat gtt ctc aaa ggg gcc cca cct ctt gtc gtt 432
 Ser Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val
 130 135 140
 cag ctg act tgg ctt aga gat gga gcc gca gcg ctc ggt att ggc ttt 480
 Gln Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe
 145 150 155
 aac cat tgt gtt tgc gat ggt atc ggc agc gcc gag ttc ctc aac ttg 528
 Asn His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu
 160 165 170 175
 ttt act gag tta tgt acg agc cgt cat aac gaa ctg ggt ggt ggc cat 576
 Phe Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His
 180 185 190

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Ser Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser	
195 200 205	
tca cgt caa cag cat gca gat aca cgt gcc agc tca gtg agt cac ctg	672
Ser Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu	
210 215 220	
gaa ttc aac aga gtg gct gat ctt tgt ggt ttt gtt tct cgt ttt tcc	720
Glu Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser	
225 230 235	
aac gaa agg ctt gtt ccc act tca ata acg ttc gat aaa cga cgc tta	768
Asn Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu	
240 245 250 255	
aac gag ctg cgg aag ctg gct ctg tcc acg agt cga ccc agt gag ctg	816
Asn Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu	
260 265 270	
gct tac acg tca ttt gaa gtt ctt tca gct cat gtg tgg aga agc tgg	864
Ala Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp	
275 280 285	
gct agg tcg ttg aat ctt ccg tcg aat caa atc ttg aag ctt cta ttt	912
Ala Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe	
290 295 300	
agc atc aat gta cgt aac cgt gtc aag ccg agt ctc ccc agt ggc tat	960
Ser Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr	
305 310 315	
tat ggc gat gca ttt gta tta ggc tgt gct caa acg agg gtt aaa gat	1008
Tyr Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp	
320 325 330 335	
ttg aca gag aag gac tta ggg cat gca gca atg ttg gtt aaa aag gcg	1056
Leu Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala	
340 345 350	
aaa gag aga gtt gat agt gag tat gtg aag tcg gtc atc gac tca gtg	1104
Lys Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val	
355 360 365	
agt cac acg aga gcg tgt ccc gac tca gtc ggg gtg ttg ata gtg tcg	1152
Ser His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser	
370 375 380	
cag tgg tca agg cta ggg tta gag aga gtt gac ttt ggg atg ggg agg	1200
Gln Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg	
385 390 395	
ccg act caa gtg ggt ccc att tgc tgc gac agg tat tgc ctg ttt cta	1248
Pro Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu	
400 405 410 415	
ccg gtt ttc aat cag acg gac gct gtt aag gtg atg gtg gcg gtc ccc	1296

Pro Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro
420 425 430

aca agt gca gtt gac aag tat gag cat ctc gcg aag ggc tta tgc tgg 1344
Thr Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
435 440 445

tgaggaccac accgcatgat gaccccacca tgtaatacgt tgacttataa actcagtttg 1404

acttttaact tttttaacaa gtgatggaat ttcagtgatt gactcatcac tttgatcctg 1464

atccaataaa taattgaatt gagttcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1520

<210> 19
<211> 455
<212> PRT
<213> Fragaria vesca

<220>
<223> Strawberry vesca alcohol acyl transferase

<400> 19
Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro
1 5 10 15

Ser Thr Ser Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
20 25 30

Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
35 40 45

Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His
50 55 60

Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
65 70 75 80

Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
85 90 95

Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys
100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile
130 135 140

Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
145 150 155 160

Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe
165 170 175

Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala
180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln
 195 200 205
 Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe
 210 215 220
 Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser
 225 230 235 240
 Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu
 245 250 255
 Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
 260 265 270
 Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
 275 280 285
 Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp
 290 295 300
 Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser
 305 310 315 320
 Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
 325 330 335
 Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr
 340 345 350
 Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
 355 360 365
 Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe
 370 375 380
 Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
 385 390 395 400
 Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
 405 410 415
 Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
 420 425 430
 Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
 435 440 445
 Lys Thr Leu Ile Ser Arg Tyr
 450 455

<210> 20
 <211> 419
 <212> PRT
 <213> Musa sp.

<220>

<223> Banana alcohol acyl transferase

<400> 20

Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
1 5 10 15

Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
20 25 30

Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
35 40 45

Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
50 55 60

Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
65 70 75 80

Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
85 90 95

Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
100 105 110

Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
115 120 125

Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
130 135 140

Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
145 150 155 160

Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
165 170 175

Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
180 185 190

Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
195 200 205

Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
210 215 220

Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
225 230 235 240

Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn
245 250 255

Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
260 265 270

His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
275 280 285

Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
 290 295 300
 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
 305 310 315 320
 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
 325 330 335
 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
 340 345 350
 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
 355 360 365
 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
 370 375 380
 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
 385 390 395 400
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
 405 410 415

Gly Phe Ala

<210> 21

<211> 454

<212> PRT

<213> Malus sp.

<220>

<223> Apple alcohol acyl transferase

<400> 21

Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile
 1 5 10 15

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
 20 25 30

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr
 35 40 45

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile
 50 55 60

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
 65 70 75 80

Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
 85 90 95

Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
 100 105 110

Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu

115	120	125
Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu		
130	135	140
Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg		
145	150	155 160
Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr		
	165	170 175
Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro		
	180	185 190
Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr		
	195	200 205
Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser		
210	215	220
Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe		
225	230	235 240
Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu		
	245	250 255
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys		
	260	265 270
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val		
	275	280 285
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro		
290	295	300
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys		
305	310	315 320
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val		
	325	330 335
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala		
	340	345 350
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser		
	355	360 365
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn		
	370	375 380
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp		
385	390	395 400
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile		
	405	410 415
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln		
	420	425 430

Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn
 435 440 445

Leu Arg Ser Thr Ser Gln
 450

<210> 22

<211> 431

<212> PRT

<213> *Mangifera indica*

<220>

<223> Mango alcohol acyl transferase

<400> 22

Met Ile Ile Thr Val Lys Glu Ser Thr Met Val Pro Pro Ser Ala Glu
 1 5 10 15

Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro
 20 25 30

Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile
 35 40 45

Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu
 50 55 60

Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly
 65 70 75 80

Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala
 85 90 95

Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu
 100 105 110

Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser
 115 120 125

Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly
 130 135 140

Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser
 145 150 155 160

Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
 165 170 175

Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp
 180 185 190

Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro
 195 200 205

Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
 210 215 220

Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
 225 230 235 240
 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
 245 250 255
 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
 260 265 270
 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
 275 280 285
 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
 290 295 300
 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
 305 310 315 320
 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
 325 330 335
 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
 340 345 350
 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
 355 360 365
 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
 370 375 380
 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
 385 390 395 400
 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
 405 410 415
 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
 420 425 430

<210> 23

<211> 426

<212> PRT

<213> Citrus limon

<220>

<223> Lemon acyl transferase

<400> 23

Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro
 1 5 10 15

Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu
 20 25 30

Thr Pro Asn Val Tyr Phe Ser Ile Ile Leu Leu Tyr Ser Lys Ala Gly
 35 40 45

Glu	Ser	Thr	Ala	Lys	Thr	Ser	Asp	His	Leu	Lys	Glu	Ser	Leu	Ser	Asn	50	55	60	
Thr	Leu	Thr	His	Tyr	Tyr	Pro	Leu	Ala	Gly	Gln	Leu	Lys	Tyr	Asp	Gln	65	70	75	80
Leu	Ile	Val	Asp	Cys	Asn	Asp	Gln	Gly	Val	Pro	Phe	Ile	Glu	Ala	His	85	90	95	
Val	Thr	Asn	Asp	Met	Arg	Gln	Leu	Leu	Lys	Ile	Pro	Asn	Ile	Asp	Val	100	105	110	
Leu	Glu	Gln	Leu	Leu	Pro	Phe	Lys	Pro	His	Glu	Gly	Phe	Asp	Ser	Asp	115	120	125	
Arg	Ser	Asn	Leu	Thr	Val	Gln	Val	Asn	Tyr	Phe	Gly	Cys	Glu	Gly	Met	130	135	140	
Ala	Ile	Gly	Leu	Cys	Phe	Arg	His	Lys	Val	Ile	Asp	Ala	Thr	Thr	Ala	145	150	155	160
Ala	Phe	Phe	Val	Lys	Asn	Trp	Gly	Val	Ile	Ala	Arg	Gly	Ala	Gly	Glu	165	170	175	
Ile	Lys	Asp	Val	Ile	Ile	Asp	His	Ala	Ser	Leu	Phe	Pro	Ala	Arg	Asp	180	185	190	
Leu	Ser	Cys	Leu	Thr	Lys	Ser	Val	Asp	Glu	Glu	Phe	Leu	Lys	Pro	Glu	195	200	205	
Ser	Glu	Thr	Lys	Arg	Phe	Val	Phe	Asp	Gly	Ala	Thr	Ile	Ala	Ser	Leu	210	215	220	
Gln	Glu	Thr	Phe	Ala	Ser	Phe	Glu	Arg	Arg	Pro	Thr	Arg	Phe	Glu	Val	225	230	235	240
Val	Ser	Ala	Val	Ile	Leu	Gly	Ala	Leu	Ile	Thr	Ala	Thr	Arg	Glu	Ser	245	250	255	
Asp	Asp	Glu	Ser	Asn	Val	Pro	Glu	Arg	Leu	Asp	Thr	Ile	Ile	Ser	Val	260	265	270	
Asn	Leu	Arg	Gln	Arg	Met	Asn	Pro	Pro	Phe	Pro	Glu	His	Cys	Met	Gly	275	280	285	
Asn	Ile	Ile	Ser	Gly	Gly	Leu	Val	Tyr	Trp	Pro	Leu	Glu	Lys	Lys	Val	290	295	300	
Asp	Tyr	Gly	Cys	Leu	Ala	Lys	Glu	Ile	His	Glu	Ser	Ile	Lys	Lys	Val	305	310	315	320
Asp	Asp	Gln	Phe	Ala	Arg	Lys	Phe	Tyr	Gly	Asp	Ala	Glu	Phe	Leu	Asn	325	330	335	
Leu	Pro	Arg	Leu	Ala	Gly	Ala	Glu	Asp	Val	Lys	Lys	Arg	Glu	Phe	Trp	340	345	350	

Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp
 355 360 365

Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr
 370 375 380

Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly
 385 390 395 400

Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu
 405 410 415

Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe
 420 425

<210> 24

<211> 491

<212> PRT

<213> Citrus limon

<220>

<223> Lemon acyl transferase

<400> 24

Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr
 1 5 10 15

Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr
 20 25 30

Leu Asp Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val
 35 40 45

Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe
 50 55 60

Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu
 65 70 75 80

Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala
 85 90 95

Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser
 100 105 110

Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His
 115 120 125

Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val
 130 135 140

Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln
 145 150 155 160

Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His
 165 170 175

His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp
 180 185 190
 Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser
 195 200 205
 Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr
 210 215 220
 Gly Gln Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn
 225 230 235 240
 Ser Asp Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp
 245 250 255
 Ser Glu Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg
 260 265 270
 Glu Asp Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys
 275 280 285
 Ser Ser Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu
 290 295 300
 Ala Tyr Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys
 305 310 315 320
 Thr Glu Ala Glu Ala Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile
 325 330 335
 Val Gly Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro
 340 345 350
 Leu Asn Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys
 355 360 365
 Ala Ser Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met
 370 375 380
 Leu Ser Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn
 385 390 395 400
 Asp Asp Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met
 405 410 415
 Ile Phe Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp
 420 425 430
 Phe Gly Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg
 435 440 445
 Thr Gln Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Gly Val
 450 455 460
 Glu Val Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser
 465 470 475 480

Val Phe Ala Asp Gly Leu Lys Asn Asp Leu Val
485 490

<210> 25
<211> 447
<212> PRT
<213> Citrus limon

<220>
<223> Lemon acyl transferase

<400> 25
Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro
1 5 10 15
Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp Ser
20 25 30
Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg Pro
35 40 45
Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser Ala
50 55 60
Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val Arg
65 70 75 80
Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly Gln
85 90 95
Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr Asp
100 105 110
Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu Ser
115 120 125
Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val Gln
130 135 140
Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn
145 150 155 160
His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe
165 170 175
Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly Gly His Ser
180 185 190
Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser Ser
195 200 205
Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu
210 215 220
Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser Asn
225 230 235 240

Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn
 245 250 255
 Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu Ala
 260 265 270
 Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala
 275 280 285
 Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe Ser
 290 295 300
 Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr
 305 310 315 320
 Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu
 325 330 335
 Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys
 340 345 350
 Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser
 355 360 365
 His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln
 370 375 380
 Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro
 385 390 395 400
 Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro
 405 410 415
 Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr
 420 425 430
 Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
 435 440 445

<210> 26

<211> 456

<212> PRT

<213> Cucumis melo

<220>

<223> Honey dew melon alcohol acyl transferase

<400> 26

Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
 1 5 10 15

Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
 20 25 30

Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
 35 40 45

His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
 50 55 60

Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
 65 70 75 80

Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
 85 90 95

Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
 100 105 110

Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
 115 120 125

Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Leu Ile
 130 135 140

Gln Val Thr Arg Leu Lys Cys Gly Gly Phe Ile Phe Gly Leu Cys Phe
 145 150 155 160

Asn His Thr Met Ala Asp Gly Phe Gly Ile Val Gln Phe Met Lys Ala
 165 170 175

Thr Ala Glu Ile Ala Arg Gly Ala Phe Ala Pro Ser Ile Leu Pro Val
 180 185 190

Trp Gln Arg Ala Leu Leu Thr Ala Arg Asp Pro Pro Arg Ile Thr Phe
 195 200 205

Arg His Tyr Glu Tyr Asp Gln Val Val Asp Met Lys Ser Gly Leu Ile
 210 215 220

Pro Val Asn Ser Lys Ile Asp Gln Leu Phe Phe Phe Ser Gln Leu Gln
 225 230 235 240

Ile Ser Thr Leu Arg Gln Thr Leu Pro Ala His Leu His Asp Cys Pro
 245 250 255

Ser Phe Glu Val Leu Thr Ala Tyr Val Trp Arg Leu Arg Thr Ile Ala
 260 265 270

Leu Gln Phe Lys Pro Glu Glu Glu Val Arg Phe Leu Cys Val Met Asn
 275 280 285

Leu Arg Ser Lys Ile Asp Ile Pro Leu Gly Tyr Tyr Gly Asn Ala Val
 290 295 300

Val Val Pro Ala Val Ile Thr Thr Ala Ala Lys Leu Cys Gly Asn Pro
 305 310 315 320

Leu Gly Tyr Ala Val Asp Leu Ile Arg Lys Ala Lys Ala Lys Ala Thr
 325 330 335

Met Glu Tyr Ile Lys Ser Thr Val Asp Leu Met Val Ile Lys Gly Arg
 340 345 350

Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg
 355 360 365

Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly
 370 375 380

Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe
 385 390 395 400

Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser
 405 410 415

Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His
 420 425 430

Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met
 435 440 445

Gln Thr Ile Gln Ser Ala Ser Lys
 450 455

<210> 27
 <211> 397
 <212> PRT
 <213> Fragaria x ananassa

<220>
 <223> Strawberry aminotransferase

<400> 27

Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro Glu Ile Ala Arg Arg
 1 5 10 15

Arg Asn Ala His Leu Gln Lys His Pro Asp Ala Lys Ile Ile Pro Leu
 20 25 30

Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala
 35 40 45

Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly
 50 55 60

Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys
 65 70 75 80

Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser
 85 90 95

Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala
 100 105 110

Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp
 115 120 125

Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln
 130 135 140

Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe
 145 150 155 160
 Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys
 165 170 175
 Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr
 180 185 190
 Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp
 195 200 205
 Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe
 210 215 220
 Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser
 225 230 235 240
 Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro
 245 250 255
 Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn
 260 265 270
 Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala
 275 280 285
 Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly
 290 295 300
 Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe
 305 310 315 320
 Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val
 325 330 335
 Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile
 340 345 350
 Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro
 355 360 365
 Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn
 370 375 380
 Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys
 385 390 395

<210> 28

<211> 458

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry thiolase

<400> 28

Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg
 1 5 10 15
 Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala
 20 25 30
 Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp
 35 40 45
 Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg
 50 55 60
 Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu
 65 70 75 80
 Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp
 85 90 95
 Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu
 100 105 110
 Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val
 115 120 125
 Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp
 130 135 140
 Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala
 145 150 155 160
 Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val
 165 170 175
 Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro
 180 185 190
 Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg
 195 200 205
 Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala
 210 215 220
 Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr
 225 230 235 240
 Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser
 245 250 255
 Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu
 260 265 270
 Lys Pro Val Phe Lys Lys Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser
 275 280 285
 Gln Val Ser Asp Gly Ala Gly Ala Val Leu Leu Met Lys Arg Ser Val
 290 295 300

Ala Asp Gln Lys Gly Leu Pro Ile Leu Gly Val Phe Arg Asn Phe Val
 305 310 315 320

Ala Val Gly Val Asp Pro Ala Ile Met Gly Val Gly Pro Ala Ala Ala
 325 330 335

Ile Pro Val Ala Val Lys Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp
 340 345 350

Leu Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg
 355 360 365

Asn Lys Leu Gly Leu Asp Pro Glu Lys Ile Asn Val Asn Gly Gly Ala
 370 375 380

Met Ala Ile Gly His Pro Leu Gly Ala Thr Gly Ala Arg Cys Val Ala
 385 390 395 400

Thr Leu Leu His Glu Met Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly
 405 410 415

Val Ile Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala Ala Val Phe
 420 425 430

Glu Arg Gly Asp Arg Thr Asp Glu Leu Cys Asn Ala Arg Lys Val Glu
 435 440 445

Ser Leu Asn Phe Leu Ser Lys Asp Val Arg
 450 455

<210> 29

<211> 605

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry pyruvate decarboxylase

<400> 29

Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His
 1 5 10 15

Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser
 20 25 30

Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His
 35 40 45

Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val
 50 55 60

Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro
 65 70 75 80

Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala
 85 90 95

Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr
 100 105 110
 Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr
 115 120 125
 Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn
 130 135 140
 Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp
 145 150 155 160
 Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala
 165 170 175
 Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile
 180 185 190
 Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys
 195 200 205
 Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro
 210 215 220
 Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala
 225 230 235 240
 Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met
 245 250 255
 Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val
 260 265 270
 Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala
 275 280 285
 Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp
 290 295 300
 Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp
 305 310 315 320
 Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly
 325 330 335
 Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp
 340 345 350
 Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys
 355 360 365
 Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala
 370 375 380
 His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys
 385 390 395 400

Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile
 405 410 415
 Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp
 420 425 430
 Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr
 435 440 445
 Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr
 450 455 460
 Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile
 465 470 475 480
 Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile
 485 490 495
 Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr
 500 505 510
 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn
 515 520 525
 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys
 530 535 540
 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile
 545 550 555 560
 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val
 565 570 575
 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser
 580 585 590
 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln
 595 600 605

<210> 30

<211> 333

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry alcohol dehydrogenase

<400> 30

Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp
 1 5 10 15

Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg
 20 25 30

Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly
 35 40 45
 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser
 50 55 60
 Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu
 65 70 75 80
 Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val
 85 90 95
 Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His
 100 105 110
 Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr
 115 120 125
 Tyr Asp Gly Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala
 130 135 140
 Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly
 145 150 155 160
 Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg
 165 170 175
 Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu
 180 185 190
 Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val
 195 200 205
 Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Arg
 210 215 220
 Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln
 225 230 235 240
 Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser
 245 250 255
 Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly
 260 265 270
 Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val
 275 280 285
 Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly
 290 295 300
 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn
 305 310 315 320
 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 325 330

<210> 31

<211> 326
 <212> PRT
 <213> Fragaria x ananassa

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 31

Glu	Thr	Gly	Ala	Thr	Asp	Val	Arg	Phe	Lys	Val	Leu	Tyr	Cys	Gly	Val	1	5	10	15
Cys	His	Ser	Asp	Ile	His	Met	Ala	Lys	Asn	Asp	Trp	Gly	Thr	Ser	Thr	20	25	30	
Tyr	Pro	Ile	Val	Pro	Gly	His	Glu	Leu	Val	Gly	Val	Val	Thr	Glu	Val	35	40	45	
Gly	Cys	Lys	Val	Lys	Lys	Phe	Lys	Ser	Trp	Arg	Gln	Gly	Arg	Cys	Trp	50	55	60	
Leu	His	Gly	Arg	Leu	Arg	Pro	Thr	Cys	Glu	Asn	Cys	Ile	His	His	Leu	65	70	75	80
Glu	Asn	Tyr	Cys	Pro	Asn	Leu	Ile	Gln	Thr	Tyr	Gly	Ser	Lys	Tyr	Tyr	85	90	95	
Asp	Gly	Thr	Met	Thr	Tyr	Gly	Gly	Tyr	Ser	Asn	Asn	Met	Val	Thr	Asp	100	105	110	
Glu	His	Phe	Ile	Val	Arg	Ile	Pro	Asp	Asn	Leu	Pro	Leu	Asp	Gly	Ala	115	120	125	
Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Trp	Arg	Tyr	130	135	140	
Tyr	Gly	Leu	Asp	Lys	Pro	Gly	Met	His	Leu	Gly	Val	Glu	Trp	Pro	Arg	145	150	155	160
Arg	Phe	Arg	Ser	Arg	Pro	Pro	Leu	Asn	Leu	Pro	Gly	Leu	Trp	Gly	Ser	165	170	175	
Arg	Leu	Gln	Ser	Leu	Val	Pro	Pro	Leu	Ile	Lys	Glu	Gly	Gly	Ser	Tyr	180	185	190	
Gly	Thr	Ser	Pro	Ala	Leu	Met	His	Ser	Leu	Leu	Arg	Thr	Asp	Gln	Asp	195	200	205	
Gln	Met	Glu	Ala	Ala	Met	Ser	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val	210	215	220	
Pro	Ala	Val	Arg	Pro	Leu	Glu	Pro	Leu	Ile	Ser	Leu	Leu	Lys	Thr	Asn	225	230	235	240
Gly	Lys	Val	Val	Thr	Val	Gly	Ile	Ala	Val	Gln	Pro	Leu	Asp	Leu	Pro	245	250	255	
Val	Phe	Pro	Leu	Ile	Ile	Gly	Arg	Lys	Met	Val	Ala	Gly	Ser	Ala	Ile				

260 265 270
 Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His
 275 280 285
 Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr
 290 295 300
 Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile
 305 310 315 320
 Asp Val Glu Asn Thr Leu
 325
 <210> 32
 <211> 278
 <212> PRT
 <213> Fragaria x ananassa
 <220>
 <223> Strawberry alcohol dehydrogenase
 <400> 32
 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu
 1 5 10 15
 Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn
 20 25 30
 Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly
 35 40 45
 Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala
 50 55 60
 Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro
 65 70 75 80
 Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly
 85 90 95
 Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu
 100 105 110
 Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr
 115 120 125
 Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu
 130 135 140
 Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala
 145 150 155 160
 Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His
 165 170 175
 Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val

180	185	190
Met Val Gly Ala Pro Glu Lys	Pro Leu Glu Leu Pro Val Phe Ser Leu	
195	200	205
Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys		
210	215	220
Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala		
225	230	235
Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg		
245	250	255
Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn		
260	265	270
Thr Leu Lys Pro Ala Ile		
275		
<210> 33		
<211> 283		
<212> PRT		
<213> Fragaria x ananassa		
<220>		
<223> Strawberry alcohol dehydrogenase		
<400> 33		
Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg		
1	5	10
Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile		
20	25	30
Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr		
35	40	45
Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val		
50	55	60
Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly		
65	70	75
Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu		
85	90	95
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr		
100	105	110
Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp		
115	120	125
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala		
130	135	140
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr		
145	150	155
		160

Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
165 170 175

Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
180 185 190

Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Glu Ala Leu Lys
195 200 205

His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met
210 215 220

Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
225 230 235 240

Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
245 250 255

Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
260 265 270

Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
275 280

<210> 34

<211> 188

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry alcohol dehydrogenase

<400> 34

Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val
1 5 10 15

Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala
20 25 30

Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp
35 40 45

Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp
50 55 60

Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp
65 70 75 80

Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys
85 90 95

Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu
100 105 110

Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser
115 120 125

Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala
 130 135 140

Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 145 150 155 160

Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe
 165 170 175

Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
 180 185

<210> 35

<211> 1227

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(979)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 35

g gaa aca gga gca acg gac gta aga ttc aaa gtg ttg tac tgt gga gta 49
 Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
 1 5 10 15

tgc cat tcg gac ata cac atg gcc aaa aat gat tgg ggg act tct acc 97
 Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
 20 25 30

tat cct att gta cct ggg cat gaa ctt gtt ggt gta gta aca gaa gta 145
 Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
 35 40 45

gga tgc aaa gta aag aaa ttc aaa agt tgg aga caa ggt cgg tgt tgg 193
 Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
 50 55 60

ttg cat ggt cga ctc aga cca act tgc gaa aat tgt atc cat cac cta 241
 Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
 65 70 75 80

gaa aat tac tgt ccg aat ctg ata caa acc tac ggt tct aaa tac tac 289
 Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
 85 90 95

gac gga acc atg aca tac gga ggt tac tcg aac aac atg gtg act gat 337
 Asp Gly Thr Met Thr Tyr Gly Gly Tyr Ser Asn Asn Met Val Thr Asp
 100 105 110

gag cac ttc att gtt cgg atc ccg gac aac tta cct ctt gat ggc gct 385
 Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala

115	120	125	
gct ccg ctt cta tgt gcc ggg att aca act tac agc cca tgg aga tat			433
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr			
130	135	140	
tat gga ctt gac aaa ccc ggt atg cat ctt ggt gtt gaa tgg cct agg			481
Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg			
145	150	155	160
cgg ttt agg tca cgt ccg ccg tta aat ttg cca ggg ctt tgg ggc tca			529
Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser			
	165	170	175
agg tta cag tca tta gta cct ccc cta att aaa gaa gga ggc agc tat			577
Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr			
	180	185	190
gga aca tct ccc gcg ctg atg cat tcc ctg ctt aga act gac caa gat			625
Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp			
	195	200	205
cag atg gag gct gcc atg agc aca atg gat ggt atc att gac aca gtt			673
Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val			
	210	215	220
cct gca gtt cga cct cta gag cct ttg att tca ttg ttg aag act aat			721
Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn			
225	230	235	240
gga aaa gtt gtt acc gtt ggt ata gca gtg cag cca ctc gat ctc cca			769
Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro			
	245	250	255
gtt ttc cct ttg ata ata gga agg aag atg gta gct ggt agt gcc att			817
Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile			
	260	265	270
gga ggt atg aaa gag acg caa gag atg att gat ttt gct gct gaa cat			865
Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His			
	275	280	285
aac ata aca gct gac atc gag gtc atc ccg att gat tac ctg aac acc			913
Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr			
	290	295	300
gca atg gaa cgc gtt gtc aaa aaa gat gtc agg ttt cga ttt gtc atc			961
Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile			
305	310	315	320
gac gtt gag aac aca ttg taagtccgcc taagtttttc attcaattct			1009
Asp Val Glu Asn Thr Leu			
	325		
gttaataaga ctatgcatta atatatgact gactctccat aggatggagt tatcagtctt			1069
caaattttcta gacatatattt gtgatcaaat aaatggaatg gctttgtttt cctttttccac			1129

taagattaga ttccagttgt attgttttta aagagattga tgtttttatt aattgtaaca 1189

gtgttatcag tctaatacatt aaaaaaaaaa aaaaaaaaaa 1227

<210> 36

<211> 1063

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (3)..(836)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 36

gc	aaa	gtg	caa	aaa	ttt	aaa	gtt	gga	gac	aaa	gtt	ggt	gtt	ggg	tgc	47
	Lys	Val	Gln	Lys	Phe	Lys	Val	Gly	Asp	Lys	Val	Gly	Val	Gly	Cys	
	1				5					10					15	

ttg	gta	ggc	tca	tgc	aaa	act	tgc	gac	agc	tgt	gct	aac	gat	ttg	gag	95
Leu	Val	Gly	Ser	Cys	Lys	Thr	Cys	Asp	Ser	Cys	Ala	Asn	Asp	Leu	Glu	
				20					25						30	

aac	tac	tgc	ccc	aaa	cag	ata	cag	act	tac	ggc	gcc	aag	tac	ctt	gac	143
Asn	Tyr	Cys	Pro	Lys	Gln	Ile	Gln	Thr	Tyr	Gly	Ala	Lys	Tyr	Leu	Asp	
			35					40					45			

gga	aca	acc	aca	tac	ggc	ggt	tac	tct	gac	atc	atg	gtg	gcg	gat	gag	191
Gly	Thr	Thr	Thr	Tyr	Gly	Gly	Tyr	Ser	Asp	Ile	Met	Val	Ala	Asp	Glu	
		50					55					60				

gcc	ttt	gta	atc	cgt	att	ccg	gac	aac	ctg	cct	ctt	gag	ggt	gct	gct	239
Ala	Phe	Val	Ile	Arg	Ile	Pro	Asp	Asn	Leu	Pro	Leu	Glu	Gly	Ala	Ala	
	65					70					75					

cct	ctc	cta	tgt	gcc	gga	atc	aca	act	tac	agt	ccc	ctg	agg	tat	ttc	287
Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Leu	Arg	Tyr	Phe	
	80				85					90					95	

gga	ctt	gac	aaa	ccc	ggc	atg	cat	gtc	ggg	gtg	gtt	ggc	ctt	ggc	ggt	335
Gly	Leu	Asp	Lys	Pro	Gly	Met	His	Val	Gly	Val	Val	Gly	Leu	Gly	Gly	
				100					105					110		

tta	ggc	cat	gtc	gcg	gtg	aag	ttt	gcc	aag	gct	ttg	ggg	gtt	aat	gtc	383
Leu	Gly	His	Val	Ala	Val	Lys	Phe	Ala	Lys	Ala	Leu	Gly	Val	Asn	Val	
			115					120					125			

aca	gtg	atc	agt	acc	tcc	gct	aat	aag	aaa	gat	gaa	gct	att	aaa	cac	431
Thr	Val	Ile	Ser	Thr	Ser	Ala	Asn	Lys	Lys	Asp	Glu	Ala	Ile	Lys	His	
		130					135					140				

ctt	ggt	gct	gat	tct	ttc	ttg	gtc	agt	cgt	gac	caa	gat	cag	atg	cag	479
Leu	Gly	Ala	Asp	Ser	Phe	Leu	Val	Ser	Arg	Asp	Gln	Asp	Gln	Met	Gln	

145	150	155	
gct gcc atg gga aca ttg gac ggt atc atc gac aca gtt tcc gca gtc			527
Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val			
160	165	170	175
cac ccc ctc cca cct ttg att agt tta ttg aag gct aat gga aag ctt			575
His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu			
	180	185	190
gtt atg gtt gga gca cca gag aag cca ctt gag cta cca gtt ttt tct			623
Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser			
	195	200	205
tta ata atg gga agg aag act tta gcc ggt agt aat atc gga ggt atc			671
Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile			
	210	215	220
aag gag aca caa gag atg ata gat ttg gca gcc aaa cac aac ata acg			719
Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr			
	225	230	235
gcc gac atc gag att atc ccc atc gac tat ttg aac act gct atg gag			767
Ala Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu			
	240	245	250
cgt ctt gct aaa ggg gat gtt aga tac cgt ttt gtc atc gac atc gga			815
Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly			
	260	265	270
aac aca ttg aag ccg gcc att taaatttgca tttcgatcag aaactgaatc			866
Asn Thr Leu Lys Pro Ala Ile			
	275		
aagcgcgaggtc gagaggcccta cgtaacaatg caaacatgtg ctagcttggt cttggagtag			926
tcttttagctt ttctctgatg tattccatct gttttgttca tgtcccatct tattatgaga			986
aaaatgtggg tacctgtgat attgaataaa tgaagagcta ctggaacgat ggtttcacaa			1046
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Ala	Arg	Asp	Ser	Ser	Gly	Val	Leu	Ser	Pro	Phe	Asn	Phe	Ser	Arg	Arg		
1				5					10					15			
gaa acc gga gag aaa gac gtt atg ttc aaa gtg ttg tac tgt gga att 96																	
Glu	Thr	Gly	Glu	Lys	Asp	Val	Met	Phe	Lys	Val	Leu	Tyr	Cys	Gly	Ile		
			20					25					30				
tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc 144																	
Cys	His	Ser	Asp	Leu	His	Met	Val	Lys	Asn	Glu	Trp	Gly	Phe	Ser	Thr		
		35					40					45					
tat cct ttg gtc ccg ggg cat gag att gtt ggt gaa gtt acg gaa gta 192																	
Tyr	Pro	Leu	Val	Pro	Gly	His	Glu	Ile	Val	Gly	Glu	Val	Thr	Glu	Val		
	50					55					60						
ggg agc aaa gta caa aaa ttt aaa gtt gga gac aga gtc ggt gtt gga 240																	
Gly	Ser	Lys	Val	Gln	Lys	Phe	Lys	Val	Gly	Asp	Arg	Val	Gly	Val	Gly		
65					70					75					80		
tgc gtt gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt 288																	
Cys	Val	Val	Gly	Ser	Cys	Arg	Ser	Cys	Glu	Asn	Cys	Thr	Asp	His	Leu		
				85					90					95			
gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac 336																	
Glu	Asn	Tyr	Cys	Pro	Lys	Gln	Ile	Leu	Thr	Tyr	Gly	Ala	Lys	Tyr	Tyr		
			100					105					110				
gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gac 384																	
Asp	Gly	Thr	Thr	Thr	Tyr	Gly	Gly	Tyr	Ser	Asp	Ile	Met	Val	Ala	Asp		
		115					120					125					
gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggc gct 432																	
Glu	His	Phe	Ile	Val	Arg	Ile	Pro	Asp	Asn	Leu	Pro	Leu	Asp	Gly	Ala		
	130					135					140						
gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat 480																	
Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr	Ser	Pro	Leu	Arg	Tyr		
145					150					155					160		
ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc 528																	
Phe	Gly	Leu	Asp	Lys	Pro	Gly	Met	His	Val	Gly	Val	Val	Gly	Leu	Gly		
			165					170						175			
ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag 576																	
Gly	Leu	Gly	His	Val	Ala	Val	Lys	Phe	Ala	Lys	Ala	Met	Gly	Val	Lys		
			180					185					190				
gtt aca gtg atc agt acg tcc cct aag aaa gag gag gaa gct ctt aaa 624																	
Val	Thr	Val	Ile	Ser	Thr	Ser	Pro	Lys	Lys	Glu	Glu	Glu	Ala	Leu	Lys		
		195					200					205					
cac cta gga gct gac tcg ttt ttc gtt agc cgt gac caa gat caa atg 672																	
His	Leu	Gly	Ala	Asp	Ser	Phe	Phe	Val	Ser	Arg	Asp	Gln	Asp	Gln	Met		
	210					215					220						
cag gct gcc att ggt acc atg gat ggg atc att gac aca gtt tct gca 720																	
Gln	Ala	Ala	Ile	Gly	Thr	Met	Asp	Gly	Ile	Ile	Asp	Thr	Val	Ser	Ala		

225	230	235	240	
caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag				768
Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys				
	245	250	255	
ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctt cca gtt ttt				816
Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe				
	260	265	270	
cct tta ctc atg gga aga aag atg ggt agc tgg taaccggcat ttgggggtat				869
Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp				
	275	280		
gaaggagaca caagagatga tagattttgc tgccaggcac aacataacag cagacatcga				929
agtcatacaa tcgactactt aaacactgct atggagcggt tagtcaaagc agatgtcaga				989
taccgttttg tcatcgacat tggaacaca ctgaaggcta gcacttaaata tctgcaatcc				1049
agactgtatc aatgaagaaa caagaacaga aactgagatt gatttggtgt catactccgc				1109
ctatgggtttt ccttacagca ttttttggtg tttgctacat gaataacgat cacatgaact				1169
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Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly				
1 5 10 15				
gtg gtt ggc ctt ggc ggt tta ggc cat gtc gcg gtg aag ttt gcc aag				95
Val Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys				
20 25 30				
gct ttg ggg gtt gag gtc aca gtg atc agt acc tcc gct aat aag aaa				143
Ala Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys				
35 40 45				
gat gaa gct att aaa cac ctt ggt gct gat tct ttc ttg gtc agt cgt				191
Asp Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg				
50 55 60				
gac caa gat cag atg cag gct gcc atg gga aca ttg gac ggt atc atc				239
Asp Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile				

65	70	75	
gac aca gtt tct gca gtc cac ccc ctc cca cct ttg att agt tta ttg			287
Asp Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu			
80	85	90	95
aag gct aat gga aag ctt gtt atg gtt gga gca cca gag aag cca ctt			335
Lys Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu			
	100	105	110
gag cta cca gtt ttt tct tta ata atg gga agg aag act tta gcc ggt			383
Glu Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly			
	115	120	125
agt aat atc gga ggt atc aag gag aca caa gag atg ata gat ttg gca			431
Ser Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala			
	130	135	140
gct aaa cac aac ata acg gcc gac atc gag gtc atc ccc atc gat tat			479
Ala Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr			
	145	150	155
ttg aac act gca atg gag cgt ctt gct aaa ggg gat gtt aga tac cgg			527
Leu Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg			
	160	165	170
ttt gtc atc gac atc gga aac aca ttg aag ccg gcc act taaatttgca			576
Phe Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr			
	180	185	
tttcgatcag aaactgaatc aagcgatgtc gagaggccta cgtaacaatg taaacatgtg			636
ctagcttggtt cttgtagtag tcttttagcat ttctctgatg tactccttct gttttgttca			696
tggtccatct tataataaga ttcttattat gaaaaaata tggtaccgtg gatattgaat			756
aaatgaagaa ctactggaac aatgggtttca caaattatgtt gtgggtgctaa aaaaaaaaaa			816
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa			852
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Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly			
1	5	10	15
Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His			
	20	25	30
Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu			
	35	40	45

His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met
50 55 60

Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val
65 70 75 80

Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys
85 90 95

Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro
100 105 110

Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly Glu
115 120 125

His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala
130 135 140

Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe
145 150 155 160

Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys
165 170 175

Cys Arg Gln Gln Ser
180

<210> 40

<211> 176

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry alcohol dehydrogenase

<400> 40

Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
1 5 10 15

Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
20 25 30

Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
35 40 45

Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
50 55 60

Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
65 70 75 80

Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
85 90 95

Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
100 105 110

Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
115 120 125

Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
130 135 140

Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
145 150 155 160

Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
165 170 175

<210> 41

<211> 283

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry alcohol dehydrogenase

<400> 41

Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
1 5 10 15

Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
20 25 30

Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
35 40 45

Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
50 55 60

Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
65 70 75 80

Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
85 90 95

Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
100 105 110

Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
115 120 125

Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
130 135 140

Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
145 150 155 160

Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
165 170 175

Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
180 185 190

Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
 195 200 205

Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
 210 215 220

Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
 225 230 235 240

Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
 245 250 255

Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
 260 265 270

Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
 275 280

<210> 42

<211> 1010

<212> DNA

<213> Fragaria x ananassa

<220>

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<222> (2)..(850)

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<400> 42

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 Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
 1 5 10 15

gcc aac aaa ggg att gga ctt gag att agc aag caa tta gct gct aaa 97
 Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
 20 25 30

gga gtt ggg gtg gta tta aca gca aga gat gtg aag aga gga aca gaa 145
 Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
 35 40 45

gct gct gaa aat ctt aag gct tct ggg ttc tct gat gtg gta ttt cat 193
 Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
 50 55 60

cag cta gat gta aca gag ccg act act att ggt tct ttg gca aac ttt 241
 Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
 65 70 75 80

ctt gaa acg caa ttt gga aag ctt gac ata ttg gtt aac aat gca gga 289
 Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
 85 90 95

gtc gtt gga tct gta tac ctc aca gcc gac tat gat cca gtg caa aca 337
 Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
 100 105 110

tac gag aca gcg agg gat tgt ttg aaa aca aac tat tat ggg ctc aag	385
Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys	
115 120 125	

caa gtc aca gaa gca ctt gtt ccg ctg ctt caa aaa tct gaa gct gca	433
Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala	
130 135 140	

agg ata gtc aat gtc tct tcc gga tta gga cag cta aga aat att gga	481
Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly	
145 150 155 160	

aat gag aag gcc aag aag gag cta gga gat gca gat aac ctc aac gag	529
Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu	
165 170 175	

gag aaa gtg gac aag cta gtt gag gaa ttt ctg gag gat gtg aaa cag	577
Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln	
180 185 190	

gat tcg ata gaa tcc aaa ggc tgg cct cta agt ata tct gcc tac att	625
Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile	
195 200 205	

gtc tca aaa gca gct ctg aat gct tat aca aga ctc ttg gca aag aag	673
Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys	
210 215 220	

tat ccc cat att gcc ata aac gca gtt ggt cca ggt tat acc aaa aca	721
Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr	
225 230 235 240	

gac ctc aat aat aat tcc ggg att ctc aca gtt gaa gaa gct gca gta	769
Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val	
245 250 255	

ggt cct gtg agg ctg gct ttg ata gcc gaa act aga att tcc ggc ctc	817
Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu	
260 265 270	

ttc ttc aac aga aat gaa gag tcg acc ttt gat taggtcaacg tgatccctga	870
Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp	
275 280	

tgaactggac tatttttagat tttcagaatg tgcttgattt tgttgaagta tttatgggat	930
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ttgtatgtat actttgatgt atcattgtat taatagagca catgttgtga tcaaaaaaaaa	990
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aaaaaaaaaa aaaaaaaaaa	1010
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<223> Mango esterase

<400> 43

Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
1 5 10 15

Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
20 25 30

Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
35 40 45

Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
50 55 60

Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
65 70 75 80

Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
85 90 95

Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
100 105 110

Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
115 120 125

Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
130 135 140

Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
145 150 155 160

Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
165 170 175

Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
180 185 190

Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
195 200 205

Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
210 215 220

Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
225 230 235 240

Ala Glu Phe

<210> 44

<211> 877

<212> DNA

<213> Mangifera indica

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<222> (1) .. (729)

<223> cDNA

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<223> Mango esterase

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ttc gga tca ggt ggt tgg ggt tct tct ctt gct gac act tac tct cgc	96
Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg	
20 25 30	
aag gct gat gta tta gtt cgt ggc tat ggt ggc tac aat act aga tgg	144
Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp	
35 40 45	
gca ttg ttc ttg tta tgt cac att ttc cct ctg cac aat aaa ata cct	192
Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro	
50 55 60	
cca gcc gtc acc aca att ttc ttt ggg gct aat gat gca gcc ctt ctt	240
Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu	
65 70 75 80	
ggg aga acg agt gaa agg cag cat gtt ccc gtg gaa gaa tac aag aac	288
Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn	
85 90 95	
aat ctc aga aaa atg gtt cag cat ttg aag gaa gtc tcc ccc acg atg	336
Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met	
100 105 110	
cta gtt gtg ctt att act cca cca cca att gat gag gaa ggg cgt aaa	384
Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys	
115 120 125	
gca tat gca cga tcc gtt tat ggt gag aaa gct atg aaa gag cct gag	432
Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu	
130 135 140	
agg aca aat gaa atg gct gga gtt tat gct aga cat tgt gtt gaa ctg	480
Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu	
145 150 155 160	
gca aaa gat ctt cct gcc att gat ctg tgg tcc aag atg cag gaa aca	528
Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr	
165 170 175	
gaa ggt tgg cag aaa aaa ttc ctc agt gat ggg ttg cac ctt aag tca	576
Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser	
180 185 190	
gaa ggc aat gca gtg gtt cac caa gaa gtt gtg aga gtt cta aaa gaa	624
Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu	

195	200	205	
gca tgg ttt tct cct gaa caa atg cca tat gat ttt cct cac caa tca			672
Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser			
210	215	220	
gta att gat gga aaa cac cct gag aaa gct ttc caa ctg caa tgc cct			720
Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro			
225	230	235	240
gct gaa ttc tagtcaagac aggcttggaa atttgttctc tctttcaatt			769
Ala Glu Phe			
tttctatttg atgaaaagat ttggactgct ttttcctagt catgccaaat gaaacagtgt			829
tagccttttg cctattttat cagatgctga tatgcgctct gtgtcgac			877
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1	5	10	
<210> 47			
<211> 16			
<212> PRT			
<213> Unknown Organism			

<220>
 <223> Description of Unknown Organism: various fruit

 <220>
 <223> alcohol acyl transferase motif

 <220>
 <221> misc_feature
 <222> (1)..(16)
 <223> Xaa is any amino acid residue

 <400> 47
 Pro Ser Arg Val Xaa Xaa Val Thr Xaa Phe Leu Xaa Lys Xaa Leu Ile
 1 5 10 15

 <210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR Primer

 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> N is Inosine

 <400> 48
 ggwtggggnk ctaytcttgc 20

 <210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR Primer

 <220>
 <223> AAP165

 <400> 49
 cggatccgga gaaaattgag gtcag 25

 <210> 50
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR Primer

 <220>
 <223> AAP166

 <400> 50

cgtcgaccat tgcacgagcc acataatc

28